

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 25, 2003, 16:05:26 ; Search time 93 Seconds

(Without alignments):
697.902 Million cell updates/sec

Title: US-09-847-809A-3

Perfect score: 1701
Sequence: 1 MDLROFLMCLSLCTAFALSK.....LFGSQATDEGALVRHDEF 315

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP-archaea:.*
2: SP-bacteria:.*
3: SP-fungi:.*
4: SP-human:.*
5: SP-invertebrate:.*
6: SP-mammal:.*
7: SP-mhc:.*
8: SP-organelle:.*
9: SP-phage:.*
10: SP-plant:.*
11: SP-rodent:.*
12: SP-virus:.*
13: SP-vertebrate:.*
14: SP-unclassified:.*
15: SP-virus:.*
16: SP-bacteriophage:.*
17: SP-archae:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1583	93.1	315	4 O96RL3	O96RL3 homo sapien
2	1516	89.1	315	11 O35783	O35783 rattus norv
3	1491	87.7	296	4 O9NR43	O9NR43 homo sapien
4	1423	83.7	296	6 O9WZ46	O9WZ46 sus scrofa
5	1031.5	60.6	322	13 O93434	O93434 fugu rubrip
6	905	53.2	322	5 O93136	O93136 bombyx mori
7	872.5	51.3	328	11 O8R137	O8R137 mus musculu
8	859.5	50.5	315	11 O99K35	O99K35 mus musculu
9	842.5	49.5	328	4 O96D15	O96D15 homo sapien
10	840.5	48.4	328	4 O9HBZ8	O9HBZ8 homo sapien
11	839.5	48.4	329	5 O8SZK6	O8SZK6 drosophila
12	779	45.8	314	5 O23017	O23017 caenorhabdi
13	742.5	43.7	259	11 O9CTD4	O9CTD4 mus musculu
14	579	34.0	321	11 O70341	O70341 mus musculu
15	564	33.2	192	5 O9W0H8	O9W0H8 drosophila
16	557.5	32.8	193	5 O96051	O96051 drosophila

17	483.5	28.4	342	5 O9VMV2	O9VMV2 drosophila
18	356.5	21.0	313	5 O9TVS8	O9TVS8 caenorhabdi
19	297.5	17.5	259	4 O96A41	O96A41 homo sapien
20	268.5	15.8	418	5 O95T97	O95T97 drosophila
21	257	15.1	391	10 O9FNNO	O9FNNO aradidopsis
22	247	14.5	348	4 O9NZP7	O9NZP7 homo sapien
23	240	14.1	261	5 O9VDY9	O9VDY9 drosophila
24	236	13.9	320	5 O18887	O18887 caenorhabdi
25	232.5	13.7	343	5 O9U460	O9U460 plasmodium
26	227.5	13.4	343	5 O25793	O25793 plasmodium
27	222	13.1	98	11 O63399	O63399 rattus norv
28	221.5	13.0	345	10 O9STP7	O9STP7 aradidopsis
29	154	9.1	482	5 O9TZ47	O9TZ47 caenorhabdi
30	154	9.1	567	5 O9TZ48	O9TZ48 caenorhabdi
31	150.5	8.8	542	5 O9NJD9	O9NJD9 onchocerca
32	146	8.6	165	5 O96609	O96609 dictyostella
33	143	8.4	531	10 O949U0	O949U0 aradidopsis
34	143	8.4	531	10 O92SA2	O92SA2 aradidopsis
35	143	8.4	1192	5 O961Z7	O961Z7 plasmodium
36	142.5	8.4	323	10 O8RWL2	O8RWL2 aradidopsis
37	142.5	8.4	521	10 O9C6P3	O9C6P3 aradidopsis
38	142	8.3	493	5 O15872	O15872 parametium
39	141.5	8.3	553	10 O80700	O80700 aradidopsis
40	141	8.3	465	10 O41793	O41793 zea mays (m
41	140.5	8.3	453	10 O9S9V0	O9S9V0 aradidopsis
42	137	8.1	163	13 O12996	O12996 xenopus lae
43	137	8.1	481	5 O18652	O18652 parametium
44	137	8.1	582	10 O9SIO7	O9SIO7 aradidopsis
45	136	8.0	540	10 O81390	O81390 nicotiana t

ALIGNMENTS

RESULT 1
ID O96RL3 PRELIMINARY: PRT; 315 AA.
AC O96RL3;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Calumenin.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Peterson R.E., Jr., Watson D.K.;
RT "Novel splice variant of human calumenin.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF345637; AAK72908.1;
DR Interpro; IPR02048; EF-hand.
DR Pfam; PF00036; efhand; 6.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_4.
SQ SEQUENCE 315 AA; 37135 MW; EIBF415B25076676 CRC64;

Query Match 93.1%; Score 1583; DB 4; Length 315;
Best Local Similarity 92.7%; Pred. No. 4.7e-93;
Matches 292; Conservative 10; Mismatches 13; Indels 0; Gaps 0;
OY 1 MDLROFLMCLSLCTAFALSKPTKRDVHHEPOLSDKVHNDASFDYDHDFAFGAEAKT 60
DB 1 MDLROFLMCLSLCTAFALSKPTKRDVHHEPOLSDKVHNDASFDYDHDFAFGAEAKT 60
OY 61 FQGLTPEESKERLGIKVSIDGKDFVYVDELDKIKRAQKRWIYEDVROWKGGDLNE 120
DB 61 FQGLTPEESKERLGIKVSIDGKDFVYVDELDKIKRAQKRWIYEDVROWKGGDLNE 120
OY 121 DGLISWDEIRNVTYIGYLLDDPPDDGFFNKQKVVRRERFRKADKDGDLIATKEETAF 180
DB 121 DGLISWDEIRNVTYIGYLLDDPPDDGFFNKQKVVRRERFRKADKDGDLIATKEETAF 180

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DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; eFhnd; 6.
DR SMART: SM00054; EFh; 2.
DR PROSITE: PS00018; EF_HAND; 4.
KM Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315 CALUMENIN.
FT CA_BIND 81 92 EF-HAND 1 (POTENTIAL).
FT CA_BIND 117 128 EF-HAND 2 (POTENTIAL).
FT CA_BIND 164 175 EF-HAND 3 (POSSIBLY ANCESTRAL).
FT CA_BIND 201 212 EF-HAND 4 (POTENTIAL).
FT CA_BIND 242 253 EF-HAND 5 (POTENTIAL).
FT CA_BIND 278 289 EF-HAND 6 (POTENTIAL).
FT CAROXYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 312 315 PREVENT SECRETION FROM ER (BY SIMILARITY).
FT CONFLICT 207 207 F -> L (IN REF. 1)
SQ SEQUENCE 315 AA; 37107 MW; 25BAE5A9B527375 CRC64;

Query Match 100.0%; Score 1701; DB 1; Length 315;
Best Local Similarity: 100.0%; Pred. No. 1.8e-94;
Matches 315; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDLROFLMCLSLCTAFALSKPTKKDRVHHEPOLSKVHNDAOSPDYDHAFLGAEEAKT 60
DB 1 MDLROFLMCLSLCTAFALSKPTKKDRVHHEPOLSKVHNDAOSPDYDHAFLGAEEAKT 60
QY 61 FQDLPEESKERLGIKIVSKIDGKDFVTVDELKDWIKFAQKRWIYEDVEROMKGDHLE 120
DB 61 FQDLPEESKERLGIKIVSKIDGKDFVTVDELKDWIKFAQKRWIYEDVEROMKGDHLE 120
QY 121 DGLVSWEEKKNAATYGVLDPPDDGFNFKOMVNRERFRKMAKDGDLIATKEEFTAF 180
DB 121 DGLVSWEEKKNAATYGVLDPPDDGFNFKOMVNRERFRKMAKDGDLIATKEEFTAF 180
QY 181 HPEEYVMDIYVQETMEDIDKNADGFIDLEEYIGMYSHDGNTDPEVWKTREGEFVE 240
DB 181 HPEEYVMDIYVQETMEDIDKNADGFIDLEEYIGMYSHDGNTDPEVWKTREGEFVE 240
QY 241 RDKNRDGMKDEETKDWILPSDYDAEAARHLVYESDONKDGKLTKEEIVDKYDLFVGS 300
DB 241 RDKNRDGMKDEETKDWILPSDYDAEAARHLVYESDONKDGKLTKEEIVDKYDLFVGS 300
QY 301 QATDFGEALVRHDEF 315
DB 301 QATDFGEALVRHDEF 315

RESULT 2
CALU_MOUSE
ID CALU_MOUSE STANDARD; PRT; 315 AA.
AC 035887;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Calumenin precursor.
GN CALU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RN SEQUENCE FROM N.A., AND CHARACTERIZATION.
RC STRAIN=ICR; TISSUE=Heart;
RC MEDLINE=97364750; PubMed=9218460;
RA Yabe D., Nakamura T., Kanazawa N., Tashiro K., Honjo T.;
RA Calumenin, a Ca2+-binding protein retained in the endoplasmic
RT reticulum with a novel carboxyl-terminal sequence. HDEF.
RL J. Biol. Chem. 272:18232-18239(1997).
CC -1- FUNCTION: NOT KNOWN, BINDS 7 CALCIUM IONS WITH A LOW AFFINITY (BY
CC similarity).
CC -1- SUBCELLULAR LOCATION: Endoplasmic reticulum lumen.
CC -1- SIMILARITY: BELONGS TO THE CREC FAMILY.

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CC -1- SIMILARITY: CONTAINS 6 EF-HAND CALCIUM-BINDING DOMAINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
DR EMBL: U81829; AAC53316.1; -.
DR MGI: 1097158; Calu.
DR InterPro: IPR002048; EF-hand.
DR Pfam: PF00036; eFhnd; 6.
DR SMART: SM00054; EFh; 2.
DR PROSITE: PS00018; EF_HAND; 4.
KM Calcium-binding; Endoplasmic reticulum; Signal; Repeat.
FT SIGNAL 1 19
FT CHAIN 20 315 CALUMENIN.
FT CA_BIND 81 92 EF-HAND 1 (POTENTIAL).
FT CA_BIND 117 128 EF-HAND 2 (POTENTIAL).
FT CA_BIND 164 175 EF-HAND 3 (POSSIBLY ANCESTRAL).
FT CA_BIND 201 212 EF-HAND 4 (POTENTIAL).
FT CA_BIND 242 253 EF-HAND 5 (POTENTIAL).
FT CA_BIND 278 289 EF-HAND 6 (POTENTIAL).
FT CAROXYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT SITE 312 315 PREVENT SECRETION FROM ER.
SQ SEQUENCE 315 AA; 37063 MW; 742361814171E273 CRC64;

Query Match 98.2%; Score 1670; DB 1; Length 315;
Best Local Similarity: 98.1%; Pred. No. 1.2e-92;
Matches 309; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MDLROFLMCLSLCTAFALSKPTKKDRVHHEPOLSKVHNDAOSPDYDHAFLGAEEAKT 60
DB 1 MDLROFLMCLSLCTAFALSKPTKKDRVHHEPOLSKVHNDAOSPDYDHAFLGAEEAKT 60
QY 61 FQDLPEESKERLGIKIVSKIDGKDFVTVDELKDWIKFAQKRWIYEDVEROMKGDHLE 120
DB 61 FQDLPEESKERLGIKIVSKIDGKDFVTVDELKDWIKFAQKRWIYEDVEROMKGDHLE 120
QY 121 DGLVSWEEKKNAATYGVLDPPDDGFNFKOMVNRERFRKMAKDGDLIATKEEFTAF 180
DB 121 DGLVSWEEKKNAATYGVLDPPDDGFNFKOMVNRERFRKMAKDGDLIATKEEFTAF 180
QY 181 HPEEYVMDIYVQETMEDIDKNADGFIDLEEYIGMYSHDGNTDPEVWKTREGEFVE 240
DB 181 HPEEYVMDIYVQETMEDIDKNADGFIDLEEYIGMYSHDGNTDPEVWKTREGEFVE 240
QY 241 RDKNRDGMKDEETKDWILPSDYDAEAARHLVYESDONKDGKLTKEEIVDKYDLFVGS 300
DB 241 RDKNRDGMKDEETKDWILPSDYDAEAARHLVYESDONKDGKLTKEEIVDKYDLFVGS 300
QY 301 QATDFGEALVRHDEF 315
DB 301 QATDFGEALVRHDEF 315

RESULT 3
RCN1_HUMAN
ID RCN1_HUMAN STANDARD; PRT; 331 AA.
AC Q15293;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Reticulocalbin 1 precursor.
GN RCN1 OR RCN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.

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QY 181 HPEEYVMYMDIVVOETMEDIDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEE 240
 DB 181 HPEEYVMYMDIVVOETMEDIDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEE 240
 QY 241 RDNKRDGKMDKEETKDWILPSDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGS 300
 DB 241 RDNKRDGKMDKEETKDWILPSDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGS 300
 QY 301 QATDFGEALVRHDEF 315
 DB 301 QATDFGEALVRHDEF 315

RESULT 2

ID 035783 PRELIMINARY; PRT; 315 AA.
 AC 035783;
 DT 01-JAN-1998 (TREMBLrel. 05, Created)
 DT 01-JUN-1998 (TREMBLrel. 05, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE CBP-50 protein.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 NC NCB1_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RA Hsueh M.J.;
 RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE-DAWLEY; TISSUE=BRAIN;
 RX MEDLINE=93107083; PubMed=8416973;
 RA Ozawa, M., Muramatsu, T.;
 RT "Retinoid-inducible: a novel endoplasmic reticulum resident calcium-binding protein with multiple EF-hand motifs and a coxoyl-terminal HDL sequence".
 RL J. Biol. Chem. 268:699-705(1993).
 DR EMBL: AJ001929; CAA05100.1;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 6.
 DR SMART: SM00054; Efh; 2.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4
 SQ SEQUENCE 315 AA; 3696 MW; 06B7FED579229B98 CRC64;

Query Match 89.1%; Score 1516; DB 11; Length 315;
 Best Local Similarity 88.6%; Pred. No. 8.3e-89;
 Matches 279; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MDLRQFLMCLSLCTAFALSKPTKKDRVHNEPOLSDKYHNDQSFYDHDHAFGLGAEBAKT 60
 DB 1 MDLRQFLMCLSLCTAFALSKPTKKDRVHNEPOLSDKYHNDQSFYDHDHAFGLGAEBAKS 60
 QY 61 FDQLTPRESKRLGKIVKIGDKDGFVYDELKDKMIFAKOKRWIYEDVEROMKGDHLE 120
 DB 61 FGQLTPRESKRLGKIVKIGDKDGFVYDELKDKMIFAKOKRWIYEDVEROMKGDHLE 120
 QY 61 FGQLTPRESKRLGKIVKIGDKDGFVYDELKDKMIFAKOKRWIYEDVEROMKGDHLE 120
 DB 61 FGQLTPRESKRLGKIVKIGDKDGFVYDELKDKMIFAKOKRWIYEDVEROMKGDHLE 120
 QY 121 DGLVMEWEKKNATYGVYLDPPDDGFNYKQAMVDERFRKADKDGDLIATKEEFTAF 180
 DB 121 DGLVMEWEKKNATYGVYLDPPDDGFNYKQAMVDERFRKADKDGDLIATKEEFTAF 180
 QY 181 HPEEYVMYMDIVVOETMEDIDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEE 240
 DB 181 HPEEYVMYMDIVVOETMEDIDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEE 240
 QY 241 RDNKRDGKMDKEETKDWILPSDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGS 300
 DB 241 RDNKRDGKMDKEETKDWILPSDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGS 300
 QY 301 QATDFGEALVRHDEF 315
 DB 301 QATDFGEALVRHDEF 315

RESULT 3

ID 09NR43 PRELIMINARY; PRT; 296 AA.
 AC 09NR43;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Crocalbin-like protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 NC NCB1_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=99192326; PubMed=10094503;
 RA Hsueh M.J., Yen C.H., Tzeng M.C.;
 RT "Crocalbin: a new calcium-binding protein that is also a binding protein for crotoxin, a neurotoxic phospholipase A2".
 RL FEBS Lett. 445:440-444(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Hsueh M.J., Tzeng M.C.;
 RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AF257659; AAF76141.1;
 DR InterPro: IPR002048; EF-hand.
 DR Pfam: PF00036; ehand; 6.
 DR SMART: SM00054; Efh; 3.
 DR PROSITE: PS00018; EF_HAND; UNKNOWN_4.
 FT NON-TER
 SQ SEQUENCE 296 AA; 34990 MW; D011D029ADEA02E CRC64;

Query Match 87.7%; Score 1491; DB 4; Length 296;
 Best Local Similarity 92.6%; Pred. No. 3e-87;
 Matches 274; Conservative 9; Mismatches 13; Indels 0; Gaps 0;

QY 20 KPTKKDRVHNEPOLSDKYHNDQSFYDHDHAFGLGAEBAKTQDLTPRESKRLGIYSK 79
 DB 1 KPTKKDRVHNEPOLSDKYHNDQSFYDHDHAFGLGAEBAKTQDLTPRESKRLGIYDK 60
 QY 80 IDGDGDFVYDELKDKMIFAKOKRWIYEDVEROMKGDHLENDGLVSWBEKKNATYGVYLD 139
 DB 61 IDADGDFVYDELKDKMIFAKOKRWIYEDVEROMKGDHLENDGLVSWBEKKNATYGVYLD 120
 QY 140 DDDPDDGFNYKQAMVDERFRKADKDGDLIATKEEFTAFHPEEYVMYMDIVVOETMED 199
 DB 121 DDDPDDGFNYKQAMVDERFRKADKDGDLIATKEEFTAFHPEEYVMYMDIVVOETMED 180
 QY 200 IDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEEFDKKNRDKMDKEETKDWIL 259
 DB 181 IDKNADGFIIDLEEYIGDMYSHDGNDEPEMYKTEREQVEEFDKKNRDKMDKEETKDWIL 240
 QY 260 PSDDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGSQATDFGEALVRHDEF 315
 DB 241 PSDDYDHAFAEARNHYVESDQNKDGKLTKEEIVDKYDLFVGSQATDFGEALVRHDEF 296
 RESULT 4
 ID 09MZ46 PRELIMINARY; PRT; 296 AA.
 AC 09MZ46;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Crocalbin-like protein (Fragment).
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 NC NCB1_TaxID=9823;
 RN [1]